

0420 03-09-01

OIPE

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/780,717

DATE: 03/05/2001  
 TIME: 12:46:27

Input Set : A:\Seqlist.txt  
 Output Set: N:\CRF3\03052001\I780717.raw

ENTERED

See p.5

4 <110> APPLICANT: Helentjaris, Tim  
 5 Bates, Nic  
 6 Allen, Stephen M.  
 8 <120> TITLE OF INVENTION: Novel Invertase Inhibitors and Methods  
 9 of Use  
 11 <130> FILE REFERENCE: 035718/208677  
 C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/780,717  
 C--> 13 <141> CURRENT FILING DATE: 2001-02-09  
 13 <150> PRIOR APPLICATION NUMBER: US 60/181,509  
 14 <151> PRIOR FILING DATE: 2000-02-10  
 16 <160> NUMBER OF SEQ ID NOS: 54  
 18 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
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 21 <211> LENGTH: 665  
 22 <212> TYPE: DNA  
 23 <213> ORGANISM: Zea mays  
 25 <220> FEATURE:  
 26 <221> NAME/KEY: CDS  
 27 <222> LOCATION: (68)...(598)  
 29 <400> SEQUENCE: 1  
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 31 ggggacc'atg aag ctt ctg caa gct ctg tgc cct ctc gtc atc ctc ctc 109  
 32 Met Lys Leu Leu Gln Ala Leu Cys Pro Leu Val Ile Leu Leu  
 33 1 5 10  
 35 gcc tgc tcc acg tcc aac gct tcc gtc cta caa gac gcg tgc aag tcc 157  
 36 Ala Cys Ser Thr Ser Asn Ala Ser Val Leu Gln Asp Ala Cys Lys Ser  
 37 15 20 25 30  
 39 ttc gcc gct aag atc ccg gac acc gcc tac gcc tac tgc atc aag ttc 205  
 40 Phe Ala Ala Lys Ile Pro Asp Thr Gly Tyr Ala Tyr Cys Ile Lys Phe  
 41 35 40 45  
 43 ttc cag gcc gac agg gga agc gcc gcc gcg gac aag cgt gcc ctc gcc 253  
 44 Phe Gln Ala Asp Arg Gly Ser Ala Gly Ala Asp Lys Arg Gly Leu Ala  
 45 50 55 60  
 47 gcc atc gcc gtg agg atc atg ggg gca gcc gcc aag agc acc gcc agt 301  
 48 Ala Ile Ala Val Arg Ile Met Gly Ala Ala Ala Lys Ser Thr Ala Ser  
 49 65 70 75  
 51 cac atc gcc gcc ctg ccg gcc tcc gag aag gac aag gag cgg ctg gcg 349  
 52 His Ile Ala Ala Leu Arg Ala Ser Glu Lys Asp Lys Glu Arg Leu Ala  
 53 80 85 90  
 55 tgc ctc agc gat tgc tcc gag gtg tac gcg cag gcc gtg gac cag acc 397  
 56 Cys Leu Ser Asp Cys Ser Glu Val Tyr Ala Gln Ala Val Asp Gln Thr  
 57 95 100 105 110  
 59 gcc gtg gcg gcg aag gcc atc gcc tcg gcc acg ccc cgg gcc cgc gcg 445  
 60 Gly Val Ala Ala Lys Gly Ile Ala Ser Gly Thr Pro Arg Gly Arg Ala  
 61 115 120 125  
 63 gac gcg gtg atg gcg ctc agc acg gtg gag gat gcc ccc gcc acc tgt 493  
 64 Asp Ala Val Met Ala Leu Ser Thr Val Glu Asp Ala Pro Gly Thr Cys

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65          130          135          140
67 gag cag ggg ttc cag gac ctg agc gtg cgt tgc ccg ctg gcc tgc gag 541
68 Glu Gln Gly Phe Gln Asp Leu Ser Val Arg Ser Pro Leu Ala Ser Glu
69          145          150          155
71 gac gcc ggg ttc cgg aag gat gcg tcc atc gcg ctg tct gta acg gcc 589
72 Asp Ala Gly Phe Arg Lys Asp Ala Ser Ile Ala Leu Ser Val Thr Ala
73          160          165          170
75 gcg ttg taa'gcaaaggtgt ataatccttt tcgatatagg ttaaaaatga 638
76 Ala Leu *
77 175
79 ataaaaaaaa aaaaaaaggc cgccgcg
81 <210> SEQ ID NO: 2
82 <211> LENGTH: 176
83 <212> TYPE: PRT
84 <213> ORGANISM: Zea mays
86 <400> SEQUENCE: 2
87 Met Lys Leu Leu Gln Ala Leu Cys Pro Leu Val Ile Leu Leu Ala Cys
88 1 5 10 15
89 Ser Thr Ser Asn Ala Ser Val Leu Gln Asp Ala Cys Lys Ser Phe Ala
90 20 25 30
91 Ala Lys Ile Pro Asp Thr Gly Tyr Ala Tyr Cys Ile Lys Phe Phe Gln
92 35 40 45
93 Ala Asp Arg Gly Ser Ala Gly Ala Asp Lys Arg Gly Leu Ala Ala Ile
94 50 55 60
95 Ala Val Arg Ile Met Gly Ala Ala Ala Lys Ser Thr Ala Ser His Ile
96 65 70 75 80
97 Ala Ala Leu Arg Ala Ser Glu Lys Asp Lys Glu Arg Leu Ala Cys Leu
98 85 90 95
99 Ser Asp Cys Ser Glu Val Tyr Ala Gln Ala Val Asp Gln Thr Gly Val
100 100 105 110
101 Ala Ala Lys Gly Ile Ala Ser Gly Thr Pro Arg Gly Arg Ala Asp Ala
102 115 120 125
103 Val Met Ala Leu Ser Thr Val Glu Asp Ala Pro Gly Thr Cys Glu Gln
104 130 135 140
105 Gly Phe Gln Asp Leu Ser Val Arg Ser Pro Leu Ala Ser Glu Asp Ala
106 145 150 155 160
107 Gly Phe Arg Lys Asp Ala Ser Ile Ala Leu Ser Val Thr Ala Ala Leu
108 165 170 175
110 <210> SEQ ID NO: 3
111 <211> LENGTH: 531
112 <212> TYPE: DNA
113 <213> ORGANISM: Zea mays
115 <400> SEQUENCE: 3
116 atgaagcttc tgcaagctct gtgccctctc gtcacccctc tcgcctgtc cagctccaac 60
117 gcttcctgc tacaagacgc gtgcaagtc ttcgccgcta agatcccga caccggctac 120
118 gcctactgca tcaagttctt ccaggccgac aggggaagcg ccggcgcgga caagcgtggc 180
119 ctcgccgcca tcgccgtgag gatcatgggg gcagccgcca agagcaccgc cagtcacatc 240
120 gccgccctgc gggcctccga gaaggacaag gagcggctgg cgtgcctcag cgattgctcc 300
121 gaggtgtacg cgcaggccgt ggaccagacc ggcgtggcgg cgaagggcat cgcctcgggc 360

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122 acgccccggg gccgcgcgga cgcggtgatg gcgctcagca cgggtggagga tgcccccggc 420
123 acctgtgagc aggggttcca ggacctgagc gtgcgttcgc cgctggcctc ggaggacgcc 480
124 gggttccgga aggatgcgtc catcgcgctg tctgtaacgg ccgcgttgta a 531
126 <210> SEQ ID NO: 4
127 <211> LENGTH: 981
128 <212> TYPE: DNA
129 <213> ORGANISM: Zea mays
131 <220> FEATURE:
132 <221> NAME/KEY: CDS
133 <222> LOCATION: (58)...(723)
135 <400> SEQUENCE: 4
136 gaattoggca cgagcatcgt ccacacaaac acatcctact ctcttttagca aaaagac atg 60
137 Met
138 1
140 gca acc acc aag agg gag aag gtc atc ctc gtc ctg ctg ttc tcc ctg 108
141 Ala Thr Thr Lys Arg Glu Lys Val Ile Leu Val Leu Leu Phe Ser Leu
142 5 10 15
144 acg atg ctc cct ctc agc acc ctc ggc acc cgc tcc ggc ccg gcg gcc 156
145 Thr Met Leu Pro Leu Ser Thr Leu Gly Thr Arg Ser Gly Pro Ala Ala
146 20 25 30
148 gtg cag cac cac ggc cac ggc ggc acc acc aag cac ccc tcg cct cct 204
149 Val Gln His His Gly His Gly Gly Thr Thr Lys His Pro Ser Pro Pro
150 35 40 45
152 tca cca gcc acg gcg gcg ctg gta cgc agc acg tgt aac tcc acg gcg 252
153 Ser Pro Ala Thr Ala Ala Leu Val Arg Ser Thr Cys Asn Ser Thr Ala
154 50 55 60 65
156 tac tac gac gtg tgc gtg tcc gcg ctg ggc gcc gac ccg tcc agc gcc 300
157 Tyr Tyr Asp Val Cys Val Ser Ala Leu Gly Ala Asp Pro Ser Ser Ala
158 70 75 80
160 acc gcc gac gtc cgc ggg ctc tcg acc atc gcc gtg tcc gcg gcg gcc 348
161 Thr Ala Asp Val Arg Gly Leu Ser Thr Ile Ala Val Ser Ala Ala Ala
162 85 90 95
164 gcc aac gcc tcg ggc ggc gcc gcc acc gcc gcg gcg ctc gcc aac ggc 396
165 Ala Asn Ala Ser Gly Gly Ala Ala Thr Ala Ala Ala Leu Ala Asn Gly
166 100 105 110
168 acc gcc acc gcg tcg tcg tcc aac gcg cag gcg gcc cct gcc acg gcc 444
169 Thr Gly Thr Ala Ser Ser Ser Asn Ala Gln Ala Ala Pro Ala Thr Ala
170 115 120 125
172 tcc gcc gcc gcg gcg ctg ctc cgc acg tgc gca gcc aag tac gcc cag 492
173 Ser Ala Ala Ala Ala Leu Leu Arg Thr Cys Ala Ala Lys Tyr Gly Gln
174 130 135 140 145
176 gcc cgg gac gcg ctg gcc gcc gcc ggg gac tcc atc gcg cag cag gac 540
177 Ala Arg Asp Ala Leu Ala Ala Ala Gly Asp Ser Ile Ala Gln Gln Asp
178 150 155 160
180 tac gac gtg gcg tcc gtg cac gtg agc gcc gcc gcc gag tac ccg cag 588
181 Tyr Asp Val Ala Ser Val His Val Ser Ala Ala Ala Glu Tyr Pro Gln
182 165 170 175
184 gtg tgt agg gtg ctg ttc cgg cgg cag aag ccc ggg cag tac ccc gcg 636
185 Val Cys Arg Val Leu Phe Arg Arg Gln Lys Pro Gly Gln Tyr Pro Ala

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186          180          185          190          684
188 gag ctg gcg gcg agg gag gag acg ctc agg cag ctc tgc tcc gtc gcg
189 Glu Leu Ala Ala Arg Glu Glu Thr Leu Arg Gln Leu Cys Ser Val Ala
190          195          200          205
192 ctc gac atc atc ggg ctc gcc tcc acc aac acc aac taa' taagctagca 733
193 Leu Asp Ile Ile Gly Leu Ala Ser Thr Asn Thr Asn *
194 210          215          220
196 gcagtgccgt ggcggcgaga aaagagagga agattaaaaa aaagtagcac ctttttcttt 793
197 ttggtttaat tactgtacgt attatattaa ttagcagggc acatgcacgc agatgcatat 853
198 ttaaaattata aaaaggttgg tgtgctgccc caatcaccgt ttgaagaatt atttgagcag 913
199 cttaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 973
200 aactcgag 981
202 <210> SEQ ID NO: 5
203 <211> LENGTH: 221
204 <212> TYPE: PRT
205 <213> ORGANISM: Zea mays
207 <400> SEQUENCE: 5
208 Met Ala Thr Thr Lys Arg Glu Lys Val Ile Leu Val Leu Leu Phe Ser
209 1          5          10          15
210 Leu Thr Met Leu Pro Leu Ser Thr Leu Gly Thr Arg Ser Gly Pro Ala
211          20          25          30
212 Ala Val Gln His His Gly His Gly Gly Thr Thr Lys His Pro Ser Pro
213          35          40          45
214 Pro Ser Pro Ala Thr Ala Ala Leu Val Arg Ser Thr Cys Asn Ser Thr
215          50          55          60
216 Ala Tyr Tyr Asp Val Cys Val Ser Ala Leu Gly Ala Asp Pro Ser Ser
217 65          70          75          80
218 Ala Thr Ala Asp Val Arg Gly Leu Ser Thr Ile Ala Val Ser Ala Ala
219          85          90          95
220 Ala Ala Asn Ala Ser Gly Gly Ala Ala Thr Ala Ala Ala Leu Ala Asn
221          100          105          110
222 Gly Thr Gly Thr Ala Ser Ser Ser Asn Ala Gln Ala Ala Pro Ala Thr
223          115          120          125
224 Ala Ser Ala Ala Ala Ala Leu Arg Thr Cys Ala Ala Lys Tyr Gly
225          130          135          140
226 Gln Ala Arg Asp Ala Leu Ala Ala Ala Gly Asp Ser Ile Ala Gln Gln
227 145          150          155          160
228 Asp Tyr Asp Val Ala Ser Val His Val Ser Ala Ala Ala Glu Tyr Pro
229          165          170          175
230 Gln Val Cys Arg Val Leu Phe Arg Arg Gln Lys Pro Gly Gln Tyr Pro
231          180          185          190
232 Ala Glu Leu Ala Ala Arg Glu Glu Thr Leu Arg Gln Leu Cys Ser Val
233          195          200          205
234 Ala Leu Asp Ile Ile Gly Leu Ala Ser Thr Asn Thr Asn
235          210          215          220
237 <210> SEQ ID NO: 6
238 <211> LENGTH: 666
239 <212> TYPE: DNA
240 <213> ORGANISM: Zea mays

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242 <400> SEQUENCE: 6
243 atggcaacca ccaagaggga gaaggtcatc ctgctcctgc tgttctccct gacgatgctc 60
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245 ggcaccacca agcacccttc gcctccttca ccagccacgg cggcgctggt acgcagcacg 180
246 tgtaactcca cggcgtaacta cgacgtgtgc gtgtccgcgc tgggcgcgca ccggtccagc 240
247 gccaccgccc agctccgccc gctctcgacc atcgccgtgt ccgcgccggc cgccaacgcc 300
248 tcgggcggcg ccgccacggc cgcggcgctc gccaacggca ccggcaccgc gtcgtcgtcc 360
249 aacgcgcagg cggcccctgc caccggcctc gccgcggcg cgtcgtcccg cactgctcga 420
250 gccaaagtacg gccaggcccc ggacgcgctg gccgcggccc gggactccat cgcgcagcag 480
251 gactacgacg tggcgctcgt gcacgtgagc gccgcggccc agtaccgcga ggtgtgtagg 540
252 gtgtgtgtcc ggcgcgagaa gcccgggcag taccgcggc agctggcgcc gagggaggag 600
253 acgctcaggg agctctgctc cgtcgcgctc gacatcatcg ggctcgcctc caccaacacc 660
254 aactaa
256 <210> SEQ ID NO: 7
257 <211> LENGTH: 779
258 <212> TYPE: DNA
259 <213> ORGANISM: Vitis L
261 <220> FEATURE:
262 <221> NAME/KEY: CDS
263 <222> LOCATION: (6)...(644)
265 <400> SEQUENCE: 7
266 ctgag atg gaa tct ttc aca tgc cta aag cta tcc tct tcc cgt ggc ctt 50
267 Met Glu Ser Phe Thr Cys Leu Lys Leu Ser Ser Ser Arg Gly Leu
268 1 5 10 15
270 gca gct att gtt gct ctc ttc ttc ttc tac ctc tca ctc aca aca cca 98
271 Ala Ala Ile Val Ala Leu Phe Phe Phe Tyr Leu Ser Leu Thr Thr Pro
272 20 25 30
274 tgc tcg gcg gcc tca cca gag ccc cat ccc cct acc aat act aca caa 146
275 Cys Ser Ala Ala Ser Pro Glu Pro His Pro Pro Thr Asn Thr Thr Gln
276 35 40 45
278 ttc atc aga acc tca tgc gga gtg act atg tac cct aag cta tgc ttc 194
279 Phe Ile Arg Thr Ser Cys Gly Val Thr Met Tyr Pro Lys Leu Cys Phe
280 50 55 60
282 aaa acc ctc tcg gct tat gcc agc acc atc caa aca agc cat atg gag 242
283 Lys Thr Leu Ser Ala Tyr Ala Ser Thr Ile Gln Thr Ser His Met Glu
284 65 70 75
286 ttg gcc aat gca gcc ctc tgt gtg agc cta aag ggc gct caa tcc tct 290
287 Leu Ala Asn Ala Ala Leu Cys Val Ser Leu Lys Gly Ala Gln Ser Ser
288 80 85 90 95
290 tca aac aag gta ctg aag tta tca aaa ggg cag ggg cta agc cgt aga 338
291 Ser Asn Lys Val Leu Lys Leu Ser Lys Gly Gln Gly Leu Ser Arg Arg
292 100 105 110
294 gaa gcc gca gcg ata acg gat tgc att gag aac atg cag gac tcg gtg 386
295 Glu Ala Ala Ala Ile Thr Asp Cys Ile Glu Asn Met Gln Asp Ser Val
296 115 120 125
298 gat gag ctc caa caa tct ctg gtg gcg atg aag gac ctt caa ggg cct 434
299 Asp Glu Leu Gln Gln Ser Leu Val Ala Met Lys Asp Leu Gln Gly Pro
300 130 135 140
302 gat ttt caa atg aaa atg agt gat ata gtg aca tgg gtg agt gca gct 482

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VERIFICATION SUMMARY  
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L:13 M:270 C: Current Application Number differs, Replaced Current Application No  
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:549 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13  
L:1592 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40